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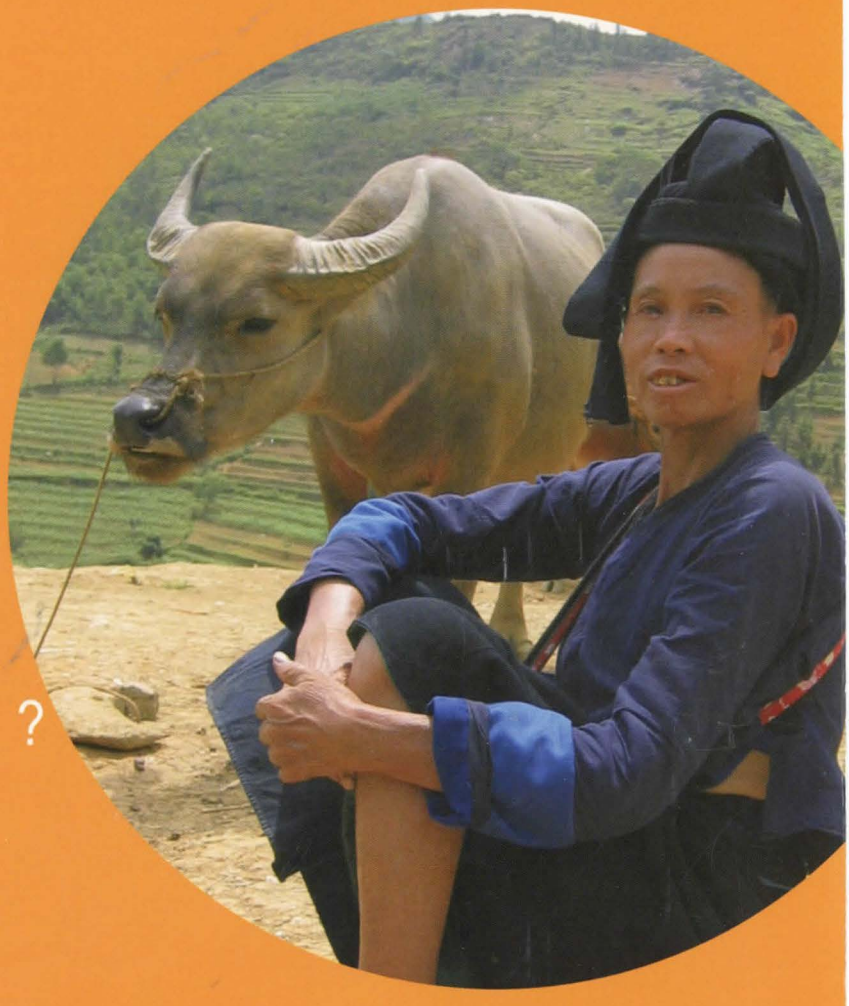

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MOLECULAR EPIDEMIOLOGY OF AFRICAN SWINE FEVER AND *PESTE DES PETITS RUMINANTS*

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ABSTRACT

African Swine Fever (ASF) and Peste des Petits Ruminants (PPR) are two highly contagious and fatal diseases of domestic pigs and small ruminants, respectively. For the control and eradication of these diseases, it is helpful to find out their origin and their mode of propagation. One of the options is the molecular tracing of the isolates based on partial genome sequencing and phylogenetic analysis. We thus performed a molecular epidemiology study on ASFV using five different genes. All of them allowed the segregation of the isolates in large regional groups, but none of them were able to discriminate at a local level. Two genes (p. 22 and p. 32) were however found to be the most variable. They were concatenated to increase distinction between local isolates. The occurrence of PPR outbreaks in three districts of Tajikistan allowed us to genetically characterize the causal strain. Partial sequence of its N protein gene was compared with the one of 43 other strains isolated since 1968 in Africa, the Middle East and Asia. The study demonstrated the value of the partial sequence of the N gene for the comparison of isolates obtained over an extended period of time and from various geographical origins.

INTRODUCTION

African Swine Fever (ASF) and Peste des Petits Ruminants (PPR) are two highly contagious and fatal diseases of domestic pigs and small ruminants, respectively. For the control and eradication of these diseases, it is helpful to find out the origin of the viruses and their mode of propagation. One of the options is the molecular tracing of the isolates based on partial genome sequencing and phylogenetic analysis.

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MATERIALS AND METHODS

For PPR, samples were collected from outbreaks and detection of PPRV RNA was performed by RT-PCR as described previously (Couacy-Hymann *et al.,* 2002). Specific PPR primers situated at the 3' end of the N gene was used and gave amplification product of 351 bp. These products were directly used for sequencing or amplified with blunted-end Cloning kit (Roche). Concerning ASFv, viral DNA was extracted from pig spleens collected during the ASF outbreak in Madagascar from 1998 to 2003. Five target genes were then amplified (VP72, p. 54, J9L, p. 22 and p. 32) and the sequencing was performed after cloning in pCR2.1 (Invitrogen).

RESULTS

The occurrence of PPR outbreaks in three districts of Tajikistan allowed us to genetically characterize the causal strain. Partial sequence of its N protein gene was compared with 43 other strains isolated since 1968 in Africa, the Middle-East and Asia. The study demonstrated the value of the partial sequence of the N gene for the comparison of isolates obtained over an extended period of time and from various geographical origins. ASFV molecular epidemiology was performed on five different genes. All of them allowed the segregation of the isolates in large regional groups, but none of them were able to discriminate at a local level. Two genes (p. 22 and p. 32) were however found to be the most variable. They were concatenated to increase distinction between local isolates.

DISCUSSION AND CONCLUSIONS

Genotypic classification based on the N-protein gene permit to distinct four PPR lineages: viruses of lineage I and II were distributed in west and central part of Africa, lineage II was located in eastern-Africa, south of Middle-East and both sides of the red sea, and lineage IV was located in the Arabian Peninsula, the Middle-East and India. Phylogenetic analysis of VP72 discriminated the isolates in 12 different groups like in previous studies (Bastos *et al.,* 2003; Lubisi *et al.,* 2005). Analysis of p54 and J9L genes were not more informative while p22 and p32 were more variable. Their concatenation allowed for the first time to pull-off the isolates within the Malagasy group but without a clear temporal and geographical discrimination.

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